



SEQUENCE LISTING

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Wood, Ken
Yu, Ming
Cytokinetics, Inc.

<120> HUMAN KINESINS AND METHODS OF PRODUCING AND PURIFYING
HUMAN KINESINS

<130> 020552-000410US

<140> 10/045,631

<141> 2001-10-19

<150> WO PCT/US00/10870

<151> 2000-04-20

<150> US 09/295,612

<151> 1999-04-20

<160> 88

<170> PatentIn Ver. 2.1

<210> 1

<211> 29

<212> DNA

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<223> Description of Artificial Sequence: 3' Primer for
amplification of Chromokinesin (residues 1-193)

<400> 1

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<223> Description of Artificial Sequence: Chromokinesin
5' Primer (spanning nucleotides 76-1178)

<400> 2

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3' Primer (spanning 76-1178)

<400> 3
gcttgacgga gagcatgctg 20

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5' Primer (spanning 1032-3326)

<400> 4
attgattacc cagttatcgg 20

<210> 5
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3' Primer (spanning 1032-3326)

<400> 5
tgatgactcc aacttcagtg 20

<210> 6
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Primer (spanning 2-2088)

<400> 6
gccgaataca tcaagcaatg gtaac 25

<210> 7
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(spanning 2-2088)

<400> 7
tctgggtatc ctttagcagc aaatg 25

<210> 8
<211> 25
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: MKLP1 5' Primer (spanning 73-2078)

<400> 8

agccatgttg tcagcgagag ctaag

25

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: MKLP1 3' Primer (spanning 73-2078)

<400> 9

agggtctctc tggcttctca gttttagg

28

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: KSP 5' Primer (spanning 66-3259)

<400> 10

ccttgatttt ttggcgggga ccgtc

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<210> 11

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: KSP 3' Primer (spanning 66-3259)

<400> 11

aaaggttgat ctgggctcgc agagg

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<210> 12

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: MCAK 5' Primer (spanning 22-2274)

<400> 12

gcgtttctct tccttgctga ctctc

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<210> 13
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 <212> DNA
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 (spanning 22-2274)

 <400> 13
 agaggctggg tgtcaaacca aacag 25

 <210> 14
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 <220>
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 (spanning 101-1596)

 <400> 14
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 <210> 15
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 (spanning 101-1596)

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 <210> 16
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 (spanning 28-248)

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 <210> 17
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 <223> Description of Artificial Sequence: Kid 3' Primer
 (spanning 28-248)

<400> 17
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<210> 18
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 (spanning 213-1624)

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<210> 19
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 (spanning 213-1624)

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<210> 20
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 (spanning 21-2311)

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 gggctccac tactgcgagg 20

<210> 21
 <211> 20
 <212> DNA
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<220>
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 (spanning 21-2311)

<400> 21
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<210> 22
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Sense oligo
 for pET23dmyc

 <400> 22
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 <210> 23
 <211> 42
 <212> DNA
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 <220>
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 <210> 24
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 tagccatgga agaggtgaag ggaattc 27

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 <210> 26
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 <400> 26
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tagaagcttc tgggtaatca attg

24

<210> 28

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: D679 5' Primer

<400> 28

tagaagcttg gaagaggtga aggg

24

<210> 29

<211> 25

<212> DNA

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<223> Description of Artificial Sequence: D679 3' Primer

<400> 29

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<210> 30

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: FL1 5' Primer

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24

<210> 31

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<223> Description of Artificial Sequence: FL1 3' Primer

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<210> 32

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 <400> 32
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 <210> 33
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 <223> Description of Artificial Sequence: P166 3' Primer

 <400> 33
 tacaagctta gcagttggat ctacagtc 28

 <210> 34
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 <212> DNA
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 <223> Description of Artificial Sequence: H195 5' Primer

 <400> 34
 tacggatcca taggatatgt gtgtgtg 27

 <210> 35
 <211> 28
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 <400> 35
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 <210> 36
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 <400> 36
 ctccatggtgta acatctttaa atgaagataa tg 32

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 <210> 39
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 <400> 39
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 <400> 40
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 <400> 41
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 <210> 42
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<223> Description of Artificial Sequence: E658 5' Primer

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<210> 43
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<400> 43
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<210> 44
<211> 31
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<400> 44
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<210> 45
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<210> 46
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<400> 46
atccatggcg tgccagccaa attcgtctgc g 31

<210> 47
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Primer

<400> 47
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<223> Description of Artificial Sequence: S553 5' Primer

<400> 48
atccatggcg tgccagccaa attcgtctgc g 31

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<400> 50
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<210> 51
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<400> 51
cactcgagca tatatttagc agtactggc 29

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<223> Description of Artificial Sequence: T340 5' Primer

<400> 52
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<400> 53
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<210> 54
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<400> 56
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<210> 57
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<210> 58
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 <223> Description of Artificial Sequence: T488 5' Primer

<400> 58
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<210> 59
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<210> 60
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<400> 60
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<210> 61
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<210> 62
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<400> 62

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<210> 63
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<400> 63
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<210> 64
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<400> 64
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<210> 65
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<400> 65
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<210> 66
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<400> 66
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<210> 67
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<400> 67
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<210> 68
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 <223> Description of Artificial Sequence: M5 5' Primer

 <400> 68
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 <210> 70
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 <400> 70
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 <210> 72
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 <400> 72
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<210> 73
 <211> 35
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 <223> Description of Artificial Sequence: FL3 3' Primer

 <400> 73
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 <210> 74
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 <223> Description of Artificial Sequence: A2N370 5' Primer

 <400> 74
 ctggatccca gccgcgggcg gctcgacgca g 31

 <210> 75
 <211> 30
 <212> DNA
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 <223> Description of Artificial Sequence: A2N370 3' Primer

 <400> 75
 cactcgagat tgatcacctc cttggacctg 30

 <210> 76
 <211> 31
 <212> DNA
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 <223> Description of Artificial Sequence: A2M511 5' Primer

 <400> 76
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 <210> 77
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 <223> Description of Artificial Sequence: A2M511 3' Primer

<400> 77
 cactcgagca ttgtgggaca atggttctc 29

<210> 78
 <211> 26
 <212> DNA
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 <223> Description of Artificial Sequence: K519 5' Primer

<400> 78
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<210> 79
 <211> 26
 <212> DNA
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 <223> Description of Artificial Sequence: K519 3' Primer

<400> 79
 cactcgagct tcctgttggc ctgagc 26

<210> 80
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 <212> DNA
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 <223> Description of Artificial Sequence: E152.2 5' Primer

<400> 80
 catgccatgg aactcaaggg caac 24

<210> 81
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 <223> Description of Artificial Sequence: E152.2 3' Primer

<400> 81
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<210> 82
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 <223> Description of Artificial Sequence: Q131.3 5'

Primer

<400> 82
ggatatccat atgcaggaac tcaagggcaa c 31

<210> 83
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<223> Description of Artificial Sequence: Q151.3 3' Primer

<400> 83
gcaggatcct cacttcctgt tggcctgag 29

<210> 84
<211> 31
<212> DNA
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<223> Description of Artificial Sequence: Q353 5' Primer

<400> 84
ctggatcccc ggggcttcgg tgaaggtggc g 31

<210> 85
<211> 30
<212> DNA
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<223> Description of Artificial Sequence: Q353 3' Primer

<400> 85
cactcgagct gcttggcccg gtcagcatatc 30

<210> 86
<211> 31
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<400> 86
ctggatcccc ggggcttcgg tgaaggtggc g 31

<210> 87
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<223> Description of Artificial Sequence: M472 3' Primer

<400> 87

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<210> 88

<211> 2663

<212> PRT

<213> Homo sapiens

<400> 88

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Asn Ser Arg Glu Glu Ser Leu Gly Glu Thr Ala Gln Val Tyr Trp Lys
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Thr Asp Asn Asn Val Ile Tyr Gln Val Asp Gly Ser Lys Ser Phe Asn
35 40 45

Phe Asp Arg Val Phe His Gly Asn Glu Thr Thr Lys Asn Val Tyr Glu
50 55 60

Glu Ile Ala Ala Pro Ile Ile Asp Ser Ala Ile Gln Gly Tyr Asn Gly
65 70 75 80

Thr Ile Phe Ala Tyr Gly Gln Thr Ala Ser Gly Lys Thr Tyr Thr Met
85 90 95

Met Gly Ser Glu Asp His Leu Gly Val Ile Pro Arg Ala Ile His Asp
100 105 110

Ile Phe Gln Lys Ile Lys Lys Phe Pro Asp Arg Glu Phe Leu Leu Arg
115 120 125

Val Ser Tyr Met Glu Ile Tyr Asn Glu Thr Ile Thr Asp Leu Leu Cys
130 135 140

Gly Thr Gln Lys Met Lys Pro Leu Ile Ile Arg Glu Asp Val Asn Arg
145 150 155 160

Asn Val Tyr Val Ala Asp Leu Thr Glu Glu Val Val Tyr Thr Ser Glu
165 170 175

Met Ala Leu Lys Trp Ile Thr Lys Gly Glu Lys Ser Arg His Tyr Gly
180 185 190

Glu Thr Lys Met Asn Gln Arg Ser Ser Arg Ser His Thr Ile Phe Arg
 195 200 205

Met Ile Leu Glu Ser Arg Glu Lys Gly Glu Pro Ser Asn Cys Glu Gly
 210 215 220

Ser Val Lys Val Ser His Leu Asn Leu Val Asp Leu Ala Gly Ser Glu
 225 230 235 240

Arg Ala Ala Gln Thr Gly Ala Ala Gly Val Arg Leu Lys Glu Gly Cys
 245 250 255

Asn Ile Asn Arg Ser Leu Phe Ile Leu Gly Gln Val Ile Lys Lys Leu
 260 265 270

Ser Asp Gly Gln Val Gly Gly Phe Ile Asn Tyr Arg Asp Ser Lys Leu
 275 280 285

Thr Arg Ile Leu Gln Asn Ser Leu Gly Gly Asn Pro Lys Thr Arg Ile
 290 295 300

Ile Cys Thr Ile Thr Pro Val Ser Phe Asp Glu Thr Leu Thr Ala Leu
 305 310 315 320

Gln Phe Ala Ser Thr Ala Lys Tyr Met Lys Asn Thr Pro Tyr Val Asn
 325 330 335

Glu Val Ser Thr Asp Glu Ala Leu Leu Lys Arg Tyr Arg Lys Glu Ile
 340 345 350

Met Asp Leu Lys Lys Gln Leu Glu Glu Val Ser Leu Glu Thr Arg Ala
 355 360 365

Gln Ala Met Glu Lys Asp Gln Leu Ala Gln Leu Leu Glu Glu Lys Asp
 370 375 380

Leu Leu Gln Lys Val Gln Asn Glu Lys Ile Glu Asn Leu Thr Arg Met
 385 390 395 400

Leu Val Thr Ser Ser Ser Leu Thr Leu Gln Gln Glu Leu Lys Ala Lys
 405 410 415

Arg Lys Arg Arg Val Thr Trp Cys Leu Gly Lys Ile Asn Lys Met Lys
 420 425 430

Asn Ser Asn Tyr Ala Asp Gln Phe Asn Ile Pro Thr Asn Ile Thr Thr

435		440		445
Lys Thr His Lys Leu Ser Ile Asn Leu Leu Arg Glu Ile Asp Glu Ser				
450		455		460
Val Cys Ser Glu Ser Asp Val Phe Ser Asn Thr Leu Asp Thr Leu Ser				
465		470		475
Glu Ile Glu Trp Asn Pro Ala Thr Lys Leu Leu Asn Gln Glu Asn Ile				
		485		490
Glu Ser Glu Leu Asn Ser Leu Arg Ala Asp Tyr Asp Asn Leu Val Leu				
		500		505
Asp Tyr Glu Gln Leu Arg Thr Glu Lys Glu Glu Met Glu Leu Lys Leu				
		515		520
Lys Glu Lys Asn Asp Leu Asp Glu Phe Glu Ala Leu Glu Arg Lys Thr				
		530		535
Lys Lys Asp Gln Glu Met Gln Leu Ile His Glu Ile Ser Asn Leu Lys				
		545		550
Asn Leu Val Lys His Arg Glu Val Tyr Asn Gln Asp Leu Glu Asn Glu				
		565		570
Leu Ser Ser Lys Val Glu Leu Leu Arg Glu Lys Glu Asp Gln Ile Lys				
		580		585
Lys Leu Gln Glu Tyr Ile Asp Ser Gln Lys Leu Glu Asn Ile Lys Met				
		595		600
Asp Leu Ser Tyr Ser Leu Glu Ser Ile Glu Asp Pro Lys Gln Met Lys				
		610		615
Gln Thr Leu Phe Asp Ala Glu Thr Val Ala Leu Asp Ala Lys Arg Glu				
		625		630
Ser Ala Phe Leu Arg Ser Glu Asn Leu Glu Leu Lys Glu Lys Met Lys				
		645		650
Glu Leu Ala Thr Thr Tyr Lys Gln Met Glu Asn Asp Ile Gln Leu Tyr				
		660		665
Gln Ser Gln Leu Glu Ala Lys Lys Lys Met Gln Val Asp Leu Glu Lys				
		675		680
				685

Glu Leu Gln Ser Ala Phe Asn Glu Ile Thr Lys Leu Thr Ser Leu Ile
 690 695 700

Asp Gly Lys Val Pro Lys Asp Leu Leu Cys Asn Leu Glu Leu Glu Gly
 705 710 715 720

Lys Ile Thr Asp Leu Gln Lys Glu Leu Asn Lys Glu Val Glu Glu Asn
 725 730 735

Glu Ala Leu Arg Glu Glu Val Ile Leu Leu Ser Glu Leu Lys Ser Leu
 740 745 750

Pro Ser Glu Val Glu Arg Leu Arg Lys Glu Ile Gln Asp Lys Ser Glu
 755 760 765

Glu Leu His Ile Ile Thr Ser Glu Lys Asp Lys Leu Phe Ser Glu Val
 770 775 780

Val His Lys Glu Ser Arg Val Gln Gly Leu Leu Glu Glu Ile Gly Lys
 785 790 795 800

Thr Lys Asp Asp Leu Ala Thr Thr Gln Ser Asn Tyr Lys Ser Thr Asp
 805 810 815

Gln Glu Phe Gln Asn Phe Lys Thr Leu His Met Asp Phe Glu Gln Lys
 820 825 830

Tyr Lys Met Val Leu Glu Glu Asn Glu Arg Met Asn Gln Glu Ile Val
 835 840 845

Asn Leu Ser Lys Glu Ala Gln Lys Phe Asp Ser Ser Leu Gly Ala Leu
 850 855 860

Lys Thr Glu Leu Ser Tyr Lys Thr Gln Glu Leu Gln Glu Lys Thr Arg
 865 870 875 880

Glu Val Gln Glu Arg Leu Asn Glu Met Glu Gln Leu Lys Glu Gln Leu
 885 890 895

Glu Asn Arg Asp Ser Pro Leu Gln Thr Val Glu Arg Glu Lys Thr Leu
 900 905 910

Ile Thr Glu Lys Leu Gln Gln Thr Leu Glu Glu Val Lys Thr Leu Thr
 915 920 925

Gln Glu Lys Asp Asp Leu Lys Gln Leu Gln Glu Ser Leu Gln Ile Glu
 930 935 940

Arg Asp Gln Leu Lys Ser Asp Ile His Asp Thr Val Asn Met Asn Ile
 945 950 955 960

Asp Thr Gln Glu Gln Leu Arg Asn Ala Leu Glu Ser Leu Lys Gln His
 965 970 975

Gln Glu Thr Ile Asn Thr Leu Lys Ser Lys Ile Ser Glu Glu Val Ser
 980 985 990

Arg Asn Leu His Met Glu Glu Asn Thr Gly Glu Thr Lys Asp Glu Phe
 995 1000 1005

Gln Gln Lys Met Val Gly Ile Asp Lys Lys Gln Asp Leu Glu Ala
 1010 1015 1020

Lys Asn Thr Gln Thr Leu Thr Ala Asp Val Lys Asp Asn Glu Ile
 1025 1030 1035

Ile Glu Gln Gln Arg Lys Ile Phe Ser Leu Ile Gln Glu Lys Asn
 1040 1045 1050

Glu Leu Gln Gln Met Leu Glu Ser Val Ile Ala Glu Lys Glu Gln
 1055 1060 1065

Leu Lys Thr Asp Leu Lys Glu Asn Ile Glu Met Thr Ile Glu Asn
 1070 1075 1080

Gln Glu Glu Leu Arg Leu Leu Gly Asp Glu Leu Lys Lys Gln Gln
 1085 1090 1095

Glu Ile Val Ala Gln Glu Lys Asn His Ala Ile Lys Lys Glu Gly
 1100 1105 1110

Glu Leu Ser Arg Thr Cys Asp Arg Leu Ala Glu Val Glu Glu Lys
 1115 1120 1125

Leu Lys Glu Lys Ser Gln Gln Leu Gln Glu Lys Gln Gln Gln Leu
 1130 1135 1140

Leu Asn Val Gln Glu Glu Met Ser Glu Met Gln Lys Lys Ile Asn
 1145 1150 1155

Glu Ile 1160	Glu Asn Leu Lys 1165	Asn Glu Leu Lys Asn Lys 1170	Glu Leu Thr
Leu Glu 1175	His Met Glu Thr Glu 1180	Arg Leu Glu Leu Ala 1185	Gln Lys Leu
Asn Glu 1190	Asn Tyr Glu Glu Val 1195	Lys Ser Ile Thr Lys 1200	Glu Arg Lys
Val Leu 1205	Lys Glu Leu Gln Lys 1210	Ser Phe Glu Thr Glu 1215	Arg Asp His
Leu Arg 1220	Gly Tyr Ile Arg Glu 1225	Ile Glu Ala Thr Gly 1230	Leu Gln Thr
Lys Glu 1235	Glu Leu Lys Ile Ala 1240	His Ile His Leu Lys 1245	Glu His Gln
Glu Thr 1250	Ile Asp Glu Leu Arg 1255	Arg Ser Val Ser Glu 1260	Lys Thr Ala
Gln Ile 1265	Ile Asn Thr Gln Asp 1270	Leu Glu Lys Ser His 1275	Thr Lys Leu
Gln Glu 1280	Glu Ile Pro Val Leu 1285	His Glu Glu Gln Glu 1290	Leu Leu Pro
Asn Val 1295	Lys Lys Val Ser Glu 1300	Thr Gln Glu Thr Met 1305	Asn Glu Leu
Glu Leu 1310	Leu Thr Glu Gln Ser 1315	Thr Thr Lys Asp Ser 1320	Thr Thr Leu
Ala Arg 1325	Ile Glu Met Glu Arg 1330	Leu Arg Leu Asn Glu 1335	Lys Phe Gln
Glu Ser 1340	Gln Glu Glu Ile Lys 1345	Ser Leu Thr Lys Glu 1350	Arg Asp Asn
Leu Lys 1355	Thr Ile Lys Glu Ala 1360	Leu Glu Val Lys His 1365	Asp Gln Leu
Lys Glu 1370	His Ile Arg Glu Thr 1375	Leu Ala Lys Ile Gln 1380	Glu Ser Gln
Ser Lys	Gln Glu Gln Ser Leu	Asn Met Lys Glu Lys	Asp Asn Glu

1385						1390						1395			
Thr	Thr	Lys	Ile	Val	Ser	Glu	Met	Glu	Gln	Phe	Lys	Pro	Lys	Asp	
1400						1405					1410				
Ser	Ala	Leu	Leu	Arg	Ile	Glu	Ile	Glu	Met	Leu	Gly	Leu	Ser	Lys	
1415						1420					1425				
Arg	Leu	Gln	Glu	Ser	His	Asp	Glu	Met	Lys	Ser	Val	Ala	Lys	Glu	
1430						1435					1440				
Lys	Asp	Asp	Leu	Gln	Arg	Leu	Gln	Glu	Val	Leu	Gln	Ser	Glu	Ser	
1445						1450					1455				
Asp	Gln	Leu	Lys	Glu	Asn	Ile	Lys	Glu	Ile	Val	Ala	Lys	His	Leu	
1460						1465					1470				
Glu	Thr	Glu	Glu	Glu	Leu	Lys	Val	Ala	His	Cys	Cys	Leu	Lys	Glu	
1475						1480					1485				
Gln	Glu	Glu	Thr	Ile	Asn	Glu	Leu	Arg	Val	Asn	Leu	Ser	Glu	Lys	
1490						1495					1500				
Glu	Thr	Glu	Ile	Ser	Thr	Ile	Gln	Lys	Gln	Leu	Glu	Ala	Ile	Asn	
1505						1510					1515				
Asp	Lys	Leu	Gln	Asn	Lys	Ile	Gln	Glu	Ile	Tyr	Glu	Lys	Glu	Glu	
1520						1525					1530				
Gln	Leu	Asn	Ile	Lys	Gln	Ile	Ser	Glu	Val	Gln	Glu	Asn	Val	Asn	
1535						1540					1545				
Glu	Leu	Lys	Gln	Phe	Lys	Glu	His	Arg	Lys	Ala	Lys	Asp	Ser	Ala	
1550						1555					1560				
Leu	Gln	Ser	Ile	Glu	Ser	Lys	Met	Leu	Glu	Leu	Thr	Asn	Arg	Leu	
1565						1570					1575				
Gln	Glu	Ser	Gln	Glu	Glu	Ile	Gln	Ile	Met	Ile	Lys	Glu	Lys	Glu	
1580						1585					1590				
Glu	Met	Lys	Arg	Val	Gln	Glu	Ala	Leu	Gln	Ile	Glu	Arg	Asp	Gln	
1595						1600					1605				
Leu	Lys	Glu	Asn	Thr	Lys	Glu	Ile	Val	Ala	Lys	Met	Lys	Glu	Ser	
1610						1615					1620				

Gln	Glu	Lys	Glu	Tyr	Gln	Phe	Leu	Lys	Met	Thr	Ala	Val	Asn	Glu
1625						1630					1635			
Thr	Gln	Glu	Lys	Met	Cys	Glu	Ile	Glu	His	Leu	Lys	Glu	Gln	Phe
1640						1645					1650			
Glu	Thr	Gln	Lys	Leu	Asn	Leu	Glu	Asn	Ile	Glu	Thr	Glu	Asn	Ile
1655						1660					1665			
Arg	Leu	Thr	Gln	Ile	Leu	His	Glu	Asn	Leu	Glu	Glu	Met	Arg	Ser
1670						1675					1680			
Val	Thr	Lys	Glu	Arg	Asp	Asp	Leu	Arg	Ser	Val	Glu	Glu	Thr	Leu
1685						1690					1695			
Lys	Val	Glu	Arg	Asp	Gln	Leu	Lys	Glu	Asn	Leu	Arg	Glu	Thr	Ile
1700						1705					1710			
Thr	Arg	Asp	Leu	Glu	Lys	Gln	Glu	Glu	Leu	Lys	Ile	Val	His	Met
1715						1720					1725			
His	Leu	Lys	Glu	His	Gln	Glu	Thr	Ile	Asp	Lys	Leu	Arg	Gly	Ile
1730						1735					1740			
Val	Ser	Glu	Lys	Thr	Asn	Glu	Ile	Ser	Asn	Met	Gln	Lys	Asp	Leu
1745						1750					1755			
Glu	His	Ser	Asn	Asp	Ala	Leu	Lys	Ala	Gln	Asp	Leu	Lys	Ile	Gln
1760						1765					1770			
Glu	Glu	Leu	Arg	Ile	Ala	His	Met	His	Leu	Lys	Glu	Gln	Gln	Glu
1775						1780					1785			
Thr	Ile	Asp	Lys	Leu	Arg	Gly	Ile	Val	Ser	Glu	Lys	Thr	Asp	Lys
1790						1795					1800			
Leu	Ser	Asn	Met	Gln	Lys	Asp	Leu	Glu	Asn	Ser	Asn	Ala	Lys	Leu
1805						1810					1815			
Gln	Glu	Lys	Ile	Gln	Glu	Leu	Lys	Ala	Asn	Glu	His	Gln	Leu	Ile
1820						1825					1830			
Thr	Leu	Lys	Lys	Asp	Val	Asn	Glu	Thr	Gln	Lys	Lys	Val	Ser	Glu
1835						1840					1845			

Met	Glu	Gln	Leu	Lys	Lys	Gln	Ile	Lys	Asp	Gln	Ser	Leu	Thr	Leu
1850						1855					1860			
Ser	Lys	Leu	Glu	Ile	Glu	Asn	Leu	Asn	Leu	Ala	Gln	Glu	Leu	His
1865						1870					1875			
Glu	Asn	Leu	Glu	Glu	Met	Lys	Ser	Val	Met	Lys	Glu	Arg	Asp	Asn
1880						1885					1890			
Leu	Arg	Arg	Val	Glu	Glu	Thr	Leu	Lys	Leu	Glu	Arg	Asp	Gln	Leu
1895						1900					1905			
Lys	Glu	Ser	Leu	Gln	Glu	Thr	Lys	Ala	Arg	Asp	Leu	Glu	Ile	Gln
1910						1915					1920			
Gln	Glu	Leu	Lys	Thr	Ala	Arg	Met	Leu	Ser	Lys	Glu	His	Lys	Glu
1925						1930					1935			
Thr	Val	Asp	Lys	Leu	Arg	Glu	Lys	Ile	Ser	Glu	Lys	Thr	Ile	Gln
1940						1945					1950			
Ile	Ser	Asp	Ile	Gln	Lys	Asp	Leu	Asp	Lys	Ser	Lys	Asp	Glu	Leu
1955						1960					1965			
Gln	Lys	Lys	Ile	Gln	Glu	Leu	Gln	Lys	Lys	Glu	Leu	Gln	Leu	Leu
1970						1975					1980			
Arg	Val	Lys	Glu	Asp	Val	Asn	Met	Ser	His	Lys	Lys	Ile	Asn	Glu
1985						1990					1995			
Met	Glu	Gln	Leu	Lys	Lys	Gln	Phe	Glu	Pro	Asn	Tyr	Leu	Cys	Lys
2000						2005					2010			
Cys	Glu	Met	Asp	Asn	Phe	Gln	Leu	Thr	Lys	Lys	Leu	His	Glu	Ser
2015						2020					2025			
Leu	Glu	Glu	Ile	Arg	Ile	Val	Ala	Lys	Glu	Arg	Asp	Glu	Leu	Arg
2030						2035					2040			
Arg	Ile	Lys	Glu	Ser	Leu	Lys	Met	Glu	Arg	Asp	Gln	Phe	Ile	Ala
2045						2050					2055			
Thr	Leu	Arg	Glu	Met	Ile	Ala	Arg	Asp	Arg	Gln	Asn	His	Gln	Val
2060						2065					2070			

Lys	Pro	Glu	Lys	Arg	Leu	Leu	Ser	Asp	Gly	Gln	Gln	His	Leu	Met
2075						2080					2085			
Glu	Ser	Leu	Arg	Glu	Lys	Cys	Ser	Arg	Ile	Lys	Glu	Leu	Leu	Lys
2090						2095					2100			
Arg	Tyr	Ser	Glu	Met	Asp	Asp	His	Tyr	Glu	Cys	Leu	Asn	Arg	Leu
2105						2110					2115			
Ser	Leu	Asp	Leu	Glu	Lys	Glu	Ile	Glu	Phe	His	Arg	Ile	Met	Lys
2120						2125					2130			
Lys	Leu	Lys	Tyr	Val	Leu	Ser	Tyr	Val	Thr	Lys	Ile	Lys	Glu	Glu
2135						2140					2145			
Gln	His	Glu	Cys	Ile	Asn	Lys	Phe	Glu	Met	Asp	Phe	Ile	Asp	Glu
2150						2155					2160			
Val	Glu	Lys	Gln	Lys	Glu	Leu	Leu	Ile	Lys	Ile	Gln	His	Leu	Gln
2165						2170					2175			
Gln	Asp	Cys	Asp	Val	Pro	Ser	Arg	Glu	Leu	Arg	Asp	Leu	Lys	Leu
2180						2185					2190			
Asn	Gln	Asn	Met	Asp	Leu	His	Ile	Glu	Glu	Ile	Leu	Lys	Asp	Phe
2195						2200					2205			
Ser	Glu	Ser	Glu	Phe	Pro	Ser	Ile	Lys	Thr	Glu	Phe	Gln	Gln	Val
2210						2215					2220			
Leu	Ser	Asn	Arg	Lys	Glu	Met	Thr	Gln	Phe	Leu	Glu	Glu	Trp	Leu
2225						2230					2235			
Asn	Thr	Arg	Phe	Asp	Ile	Glu	Lys	Leu	Lys	Asn	Gly	Ile	Gln	Lys
2240						2245					2250			
Glu	Asn	Asp	Arg	Ile	Cys	Gln	Val	Asn	Asn	Phe	Phe	Asn	Asn	Arg
2255						2260					2265			
Ile	Ile	Ala	Ile	Met	Asn	Glu	Ser	Thr	Glu	Phe	Glu	Glu	Arg	Ser
2270						2275					2280			
Ala	Thr	Ile	Ser	Lys	Glu	Trp	Glu	Gln	Asp	Leu	Lys	Ser	Leu	Lys
2285						2290					2295			
Glu	Lys	Asn	Glu	Lys	Leu	Phe	Lys	Asn	Tyr	Gln	Thr	Leu	Lys	Thr

2300		2305		2310
Ser Leu Ala Ser Gly Ala Gln Val Asn Pro Thr Thr Gln Asp Asn				
2315		2320		2325
Lys Asn Pro His Val Thr Ser Arg Ala Thr Gln Leu Thr Thr Glu				
2330		2335		2340
Lys Ile Arg Glu Leu Glu Asn Ser Leu His Glu Ala Lys Glu Ser				
2345		2350		2355
Ala Met His Lys Glu Ser Lys Ile Ile Lys Met Gln Lys Glu Leu				
2360		2365		2370
Glu Val Thr Asn Asp Ile Ile Ala Lys Leu Gln Ala Lys Val His				
2375		2380		2385
Glu Ser Asn Lys Cys Leu Glu Lys Thr Lys Glu Thr Ile Gln Val				
2390		2395		2400
Leu Gln Asp Lys Val Ala Leu Gly Ala Lys Pro Tyr Lys Glu Glu				
2405		2410		2415
Ile Glu Asp Leu Lys Met Lys Leu Val Lys Ile Asp Leu Glu Lys				
2420		2425		2430
Met Lys Asn Ala Lys Glu Phe Glu Lys Glu Ile Ser Ala Thr Lys				
2435		2440		2445
Ala Thr Val Glu Tyr Gln Lys Glu Val Ile Arg Leu Leu Arg Glu				
2450		2455		2460
Asn Leu Arg Arg Ser Gln Gln Ala Gln Asp Thr Ser Val Ile Ser				
2465		2470		2475
Glu His Thr Asp Pro Gln Pro Ser Asn Lys Pro Leu Thr Cys Gly				
2480		2485		2490
Gly Gly Ser Gly Ile Val Gln Asn Thr Lys Ala Leu Ile Leu Lys				
2495		2500		2505
Ser Glu His Ile Arg Leu Glu Lys Glu Ile Ser Lys Leu Lys Gln				
2510		2515		2520
Gln Asn Glu Gln Leu Ile Lys Gln Lys Asn Glu Leu Leu Ser Asn				
2525		2530		2535

Asn	Gln	His	Leu	Ser	Asn	Glu	Val	Lys	Thr	Trp	Lys	Glu	Arg	Thr
2540						2545					2550			
Leu	Lys	Arg	Glu	Ala	His	Lys	Gln	Val	Thr	Cys	Glu	Asn	Ser	Pro
2555						2560					2565			
Lys	Ser	Pro	Lys	Val	Thr	Gly	Thr	Ala	Ser	Lys	Lys	Lys	Gln	Ile
2570						2575					2580			
Thr	Pro	Ser	Gln	Cys	Lys	Glu	Arg	Asn	Leu	Gln	Asp	Pro	Val	Pro
2585						2590					2595			
Lys	Glu	Ser	Pro	Lys	Ser	Cys	Phe	Phe	Asp	Ser	Arg	Ser	Lys	Ser
2600						2605					2610			
Leu	Pro	Ser	Pro	His	Pro	Val	Arg	Tyr	Phe	Asp	Asn	Ser	Ser	Leu
2615						2620					2625			
Gly	Leu	Cys	Pro	Glu	Val	Gln	Asn	Ala	Gly	Ala	Glu	Ser	Val	Asp
2630						2635					2640			
Ser	Gln	Pro	Gly	Pro	Trp	His	Ala	Ser	Ser	Gly	Lys	Asp	Val	Pro
2645						2650					2655			
Glu	Cys	Lys	Thr	Gln										
2660														